



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/803,459A
Source: FWO
Date Processed by STIC: 7/29/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/803,459A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) 3,4,6 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 07/29/2004

PATENT APPLICATION: US/10/803,459A

TIME: 09:36:52

Input Set : D:\Leptin Sequence Listing-Corrected.txt

Output Set: N:\CRF4\07292004\J803459A.raw

3 <110> APPLICANT: Gertler, Arie
 4 Krishna, Radha G.
 6 <120> TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO
 8 <130> FILE REFERENCE: 28758.1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/803,459A
 C--> 10 <141> CURRENT FILING DATE: 2004-03-19
 10 <160> NUMBER OF SEQ ID NOS: 8
 12 <170> SOFTWARE: PatentIn version 3.2
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 630
 16 <212> TYPE: DNA
 17 <213> ORGANISM: homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(630)
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_feature
 26 <222> LOCATION: (6)..(6)
 27 <223> OTHER INFORMATION: n is a, c, g, or t
 29 <400> SEQUENCE: 1

W--> 30 atg gcn att gat gtc aat atc aat atc tca tgt gaa act gat ggg tac 48
 31 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
 32 1 5 10 15
 34 tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt 96
 35 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
 36 20 25 30
 38 gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt 144
 39 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
 40 35 40 45
 42 tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat 192
 43 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
 44 50 55 60
 46 ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta 240
 47 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
 48 65 70 75 80
 50 tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca 288
 51 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
 52 85 90 95
 54 ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca 336
 55 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
 56 100 105 110
 58 ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta 384
 59 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu

p.3
 Does Not Comply
 Corrected Diskette Reader

RAW SEQUENCE LISTING

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TIME: 09:36:52

Input Set : D:\Leptin Sequence Listing-Corrected.txt

Output Set: N:\CRF4\07292004\J803459A.raw

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60      115      120      125
62 ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa      432
63 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
64      130      135      140
66 ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg      480
67 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
68 145      150      155      160
70 tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca      528
71 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
72      165      170      175
74 gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat      576
75 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
76      180      185      190
78 gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc      624
79 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
80      195      200      205
82 atg gat      630
83 Met Asp
84      210
87 <210> SEQ ID NO: 2
88 <211> LENGTH: 210
89 <212> TYPE: PRT
90 <213> ORGANISM: homo sapiens
92 <400> SEQUENCE: 2
94 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
95 1      5      10      15
98 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
99      20      25      30
102 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
103      35      40      45
106 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
107      50      55      60
110 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
111 65      70      75      80
114 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
115      85      90      95
118 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
119      100      105      110
122 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
123      115      120      125
126 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
127      130      135      140
130 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
131 145      150      155      160
134 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
135      165      170      175
138 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
139      180      185      190
142 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val

```

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Input Set : D:\Leptin Sequence Listing-Corrected.txt

Output Set: N:\CRF4\07292004\J803459A.raw

143 195 200 205

146 Met Asp

147 210

150 <210> SEQ ID NO: 3

151 <211> LENGTH: 36

152 <212> TYPE: DNA

153 <213> ORGANISM: Artificial Sequence

155 <220> FEATURE:

W--> 156 <221> NAME/KEY:

157 <222> LOCATION:

158 <223> OTHER INFORMATION:

W--> 160 <400> 3

161 ggaattccat atgattgatg tcaatatcaa tatctc

36

164 <210> SEQ ID NO: 4

165 <211> LENGTH: 39

166 <212> TYPE: DNA

167 <213> ORGANISM: Artificial Sequence

169 <220> FEATURE:

W--> 170 <221> NAME/KEY:

171 <222> LOCATION:

172 <223> OTHER INFORMATION:

W--> 174 <400> 4

175 cataggaagc tttcaatcca tgacaactgt gtaggctgg

39

178 <210> SEQ ID NO: 5

179 <211> LENGTH: 12

180 <212> TYPE: PRT

181 <213> ORGANISM: homo sapiens

184 <220> FEATURE:

185 <221> NAME/KEY: misc_feature

186 <222> LOCATION: (11)..(11)

187 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

189 <400> SEQUENCE: 5

W--> 191 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu

192 1

5

10

195 <210> SEQ ID NO: 6

196 <211> LENGTH: 5

197 <212> TYPE: PRT

198 <213> ORGANISM: Artificial Sequence

201 <220> FEATURE:

202 <221> NAME/KEY: misc_feature

203 <222> LOCATION: (3)..(3)

204 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

206 <400> SEQUENCE: 6

W--> 208 Trp Ser Xaa Trp Ser

209 1

5

212 <210> SEQ ID NO: 7

213 <211> LENGTH: 627

214 <212> TYPE: DNA

215 <213> ORGANISM: gallus domesticus

RAW SEQUENCE LISTING

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Input Set : D:\Leptin Sequence Listing-Corrected.txt

Output Set: N:\CRF4\07292004\J803459A.raw

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218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (1)..(627)
222 <220> FEATURE:
223 <221> NAME/KEY: misc_feature
224 <222> LOCATION: (6)..(6)
225 <223> OTHER INFORMATION: n is a, c, g, or t
227 <400> SEQUENCE: 7
W--> 228 atg gcn gta gat gtg aat atc aat atc aaa tgt gaa act gat ggg tac      48
229 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
230 1          5          10          15
232 tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc      96
233 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
234          20          25          30
236 ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt      144
237 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
238          35          40          45
240 tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat      192
241 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
242          50          55          60
244 ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt      240
245 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
246 65          70          75          80
248 tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca      288
249 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
250          85          90          95
252 ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca      336
253 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
254          100          105          110
256 ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg      384
257 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
258          115          120          125
260 ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag      432
261 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
262          130          135          140
264 ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg      480
265 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
266 145          150          155          160
268 tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa      528
269 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
270          165          170          175
272 ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc      576
273 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
274          180          185          190
276 tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa      624
277 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
278          195          200          205
280 gat      627
281 Asp

```

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TIME: 09:36:52

Input Set : D:\Leptin Sequence Listing-Corrected.txt

Output Set: N:\CRF4\07292004\J803459A.raw

```

285 <210> SEQ ID NO: 8
286 <211> LENGTH: 209
287 <212> TYPE: PRT
288 <213> ORGANISM: gallus domesticus
290 <400> SEQUENCE: 8
292 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
293 1 5 10 15
296 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
297 20 25 30
300 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
301 35 40 45
304 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
305 50 55 60
308 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
309 65 70 75 80
312 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
313 85 90 95
316 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
317 100 105 110
320 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
321 115 120 125
324 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
325 130 135 140
328 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
329 145 150 155 160
332 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
333 165 170 175
336 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
337 180 185 190
340 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
341 195 200 205
344 Asp

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/29/2004
PATENT APPLICATION: US/10/803,459A TIME: 09:36:53

Input Set : D:\Leptin Sequence Listing-Corrected.txt
Output Set: N:\CRF4\07292004\J803459A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6 ✓
Seq#:5; Xaa Pos. 11 ✓
Seq#:6; Xaa Pos. 3 ✓
Seq#:7; N Pos. 6 ✓

VERIFICATION SUMMARY

DATE: 07/29/2004

PATENT APPLICATION: US/10/803,459A

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Input Set : D:\Leptin Sequence Listing-Corrected.txt

Output Set: N:\CRF4\07292004\J803459A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:156 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:158
L:170 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:174 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:172
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0